<110> ALBERTSEN, MARC C. FOX, TIM HUFFMAN, GARY TRIMNELL, MARY										
<120> NUCLEOTIDE SEQUENCES MEDIATING MALE FERTILITY AND METHOD OF USING SAME										
<130> 1148										
<140> 09/670,153 <141> 2000-09-26										
<160> 7										
<170> PatentIn Ver. 2.1										
<210> 1 <211> 1906 <212> DNA <213> Zea mays										
<220> <221> CDS <222> (11638, 16421767)										
<pre>&lt;400&gt; 1 gaa ttc ggc acg agg gaa gct cac ctc acg ccg gcg acg cca tcg cca Glu Phe Gly Thr Arg Glu Ala His Leu Thr Pro Ala Thr Pro Ser Pro</pre>	48									
ttc ttc cca cta gca ggg cct cac aag tac atc gcg ctc ctt ctg gtt Phe Phe Pro Leu Ala Gly Pro His Lys Tyr Ile Ala Leu Leu Leu Val 20 25 30	96									
gtc ctc tca tgg atc ctg gtc cag agg tgg agc ctg agg aag cag aaa Val Leu Ser Trp Ile Leu Val Gln Arg Trp Ser Leu Arg Lys Gln Lys 35 40 45	144									
ggc ccg aga tca tgg cca gtc atc ggc gca acg gtg gag cag ctg agg Gly Pro Arg Ser Trp Pro Val Ile Gly Ala Thr Val Glu Gln Leu Arg 50 55 60	192									
aac tac cac egg atg cac gac tgg ctt gtc ggg tac etg tea egg cac Asn Tyr His Arg Met His Asp Trp Leu Val Gly Tyr Leu Ser Arg His 65 70 75 80	240									
agg aca gtg acc gtc gac atg ccg ttc act tcc tac acc tac atc gct Arg Thr Val Thr Val Asp Met Pro Phe Thr Ser Tyr Thr Tyr Ile Ala  85 90 95	288									
gac ccg gtg aat gtc gag cat gtc ctc aag act aac ttc acc aat tac Asp Pro Val Asn Val Glu His Val Leu Lys Thr Asn Phe Thr Asn Tyr 100 105 110	336									

	_		atc Ile		J Tyr							ctc Leu 125				384
				_	gac Asp			-			_	_		_	_	432
					gcc Ala 150		_			22	_			_		480
			-		tcc Ser	_	_	_				_	_	-	_	528
					gtt Val											576
					tgc Cys											624
					ccc Pro						_					672
					acg Thr 230											720
_					gtc Val				_				_			768
					ttc Phe				Val							816
			Glu		cgg Arg											864
					ttc Phe							Gly			ggc Gly	912
~ ~				-	_	Lys	-				Val				ttc Phe 320	960
		_			Asp	_	_		-	Thr	_	_			acg Thr	1008

			( His								1056
			gcg Ala								1104
			gct Ala								1152
			ggc 390								1200
			tgc Cys								1248
			aag Lys								1296
			gcc Ala								1344
			tac Tyr							cgg Arg	1392
										ccg Pro 480	1440
			Phe							aag Lys	1488
		Leu								cgc Arg	1536
	Phe				Gly				Tyr	atg Met	1584
			_	 His		_	-	Arg	_	agg Arg	1632
Val				Leu				Val		aat Asn	1680

cca cga caa ata acg c gtg tta caa att tgc atg cat gca tgt aag Pro Arg Gln Ile Thr Leu Val Leu Gln Ile Cys Met His Ala Cys Lys 560 565 570 575	1728
gga aag cga tgg gtt tca ttg gtg gct tgg ctt aag cct taaaaaactcc Gly Lys Arg Trp Val Ser Leu Val Ala Trp Leu Lys Pro 580 585	1777
gtegggtett gegaaceace acateactag tgttttgtae tetacteete agtggaagtg	1837
tagtgacage atacaagtte atcatatata ttateetett tettaaaaaa aaaaaaaaaa	1897
aaactcgag	1906
<210> 2 <211> 588 <212> PRT <213> Zea mays	
<pre>&lt;400&gt; 2 Glu Phe Gly Thr Arg Glu Ala His Leu Thr Pro Ala Thr Pro Ser Pro 1 5 10 15</pre>	
Phe Phe Pro Leu Ala Gly Pro His Lys Tyr Ile Ala Leu Leu Val 20 25 30	
Val Leu Ser Trp Ile Leu Val Gln Arg Trp Ser Leu Arg Lys Gln Lys 35 40 45	
Gly Pro Arg Ser Trp Pro Val Ile Gly Ala Thr Val Glu Gln Leu Arg 50 55 60	
Asn Tyr His Arg Met His Asp Trp Leu Val Gly Tyr Leu Ser Arg His 65 70 75 80	
Arg Thr Val Thr Val Asp Met Pro Phe Thr Ser Tyr Thr Tyr Ile Ala 85 90 95	
Asp Pro Val Asn Val Glu His Val Leu Lys Thr Asn Phe Thr Asn Tyr 100 105 110	
Pro Lys Gly Ile Val Tyr Arg Ser Tyr Met Asp Val Leu Leu Gly Asp 115 120 125	
Gly Ile Phe Asn Ala Asp Gly Glu Leu Trp Arg Lys Gln Arg Lys Thr 130 135 140	
Ala Ser Phe Glu Phe Ala Ser Lys Asn Leu Arg Asp Phe Ser Ala Ile 145 150 155 160	
Val Phe Arg Glu Tyr Ser Leu Lys Leu Ser Gly Ile Leu Ser Gln Ala 165 170 175	
Ser Lys Ala Gly Lys Val Val Asp Met Gln Glu Leu Tyr Met Arg Met 180 185 190	

- Thr Leu Asp Ser Ile ( Lys Val Gly Phe Gly Val Glu Ile Gly Thr 195 200 205
- Leu Ser Pro Asp Leu Pro Glu Asn Ser Phe Ala Gln Ala Phe Asp Ala 210 215 220
- Ala Asn Ile Ile Ile Thr Leu Arg Phe Ile Asp Pro Leu Trp Arg Ile 225 230 235 240
- Lys Arg Phe Phe His Val Gly Ser Glu Ala Leu Leu Ala Gln Ser Ile
  245 250 255
- Lys Leu Val Asp Glu Phe Thr Tyr Ser Val Ile Arg Arg Lys Ala 260 265 270
- Glu Ile Val Glu Val Arg Ala Ser Gly Lys Gln Glu Lys Met Lys His 275 280 285
- Asp Ile Leu Ser Arg Phe Ile Glu Leu Gly Glu Ala Gly Asp Asp Gly 290 295 300
- Gly Gly Phe Gly Asp Asp Lys Ser Leu Arg Asp Val Val Leu Asn Phe 305 310 315 320
- Val Ile Ala Gly Arg Asp Thr Thr Ala Thr Thr Leu Ser Trp Phe Thr
  325 330 335
- His Met Ala Met Ser His Pro Asp Val Ala Glu Lys Leu Arg Arg Glu 340 345 350
- Leu Cys Ala Phe Glu Ala Glu Arg Ala Arg Glu Glu Gly Val Thr Leu 355 360 365
- Val Leu Cys Gly Gly Ala Asp Ala Asp Asp Lys Ala Phe Ala Ala Arg 370 375 380
- Val Ala Gln Phe Ala Gly Leu Leu Thr Tyr Asp Ser Leu Gly Lys Leu 385 390 395 400
- Val Tyr Leu His Ala Cys Val Thr Glu Thr Leu Arg Leu Tyr Pro Ala
  405 410 415
- Val Pro Gln Asp Pro Lys Gly Ile Leu Glu Asp Asp Val Leu Pro Asp 420 425 430
- Gly Thr Lys Val Arg Ala Gly Gly Met Val Thr Tyr Val Pro Tyr Ser 435 440 445
- Met Gly Arg Met Glu Tyr Asn Trp Gly Pro Asp Ala Ala Ser Phe Arg 450 455 460
- Pro Glu Arg Trp Ile Asn Glu Asp Gly Ala Phe Arg Asn Ala Ser Pro 465 470 475 480
- Phe Lys Phe Thr Ala Phe Gln Ala Gly Pro Arg Ile Cys Leu Gly Lys 485 490 495

```
Asp Ser Ala Tyr Leu G: Met Lys Met Ala Leu Ala Ile Leu Phe Arq
                                505
Phe Tyr Ser Phe Arg Leu Leu Glu Gly His Pro Val Gln Tyr Arg Met
                            520
Met Thr Ile Leu Ser Met Ala His Gly Leu Lys Val Arg Val Ser Arg
                        535
                                            540
Ala Val Cys His Gly Asp Leu Asp Met Asp Ile Val Pro Leu Asn Pro
                    550
Arg Gln Ile Thr Leu Val Leu Gln Ile Cys Met His Ala Cys Lys Gly
                                    570
Lys Arg Trp Val Ser Leu Val Ala Trp Leu Lys Pro
<210> 3
<211> 494
<212> DNA
<213> Sorghum sp.
<220>
<221> modified base
<222> (1)..(494)
<223> "n" bases may be a, t, c, g, other or unknown
ggaattegge ttatgeegtt cactteetae acetacateg etgaceeggt gaatgtegag 60
catgtcctca agactaactt caccaattac cccaaggggg acgtgtacag atcctacatg 120
gatgtgctcc tcggtgacgg catattcaac gctgacggcg agctgtggag gaagcagagg 180
aagacggcga qtttcgagtt cgcctccaag aacctgaggg atttcagtgc caatgttttc 240
agagagtact ccctgaagct gtcgggcata ctgagtcagg catccaagqc aggcaaaqtt 300
gttgacatgc aggaacttta catgaggatg acactggact cgatctgcaa ngttgggttc 360
ggggtenana teggeaeget gteneeggat eteecegaqa acaqettene ecaageqtte 420
gatgccgcta acatcatcgt cacnotgcgg ttcatccacc cnctqtqqcq catccaqaaq 480
ttcttccccn gtca
<210> 4
<211> 158
<212> PRT
<213> Sorghum sp.
<220>
<221> MOD RES
<222> (1)..(158)
<223> "Xaa" may be any, other or unknown amino acid
<400> 4
Met Pro Phe Thr Ser Tyr Thr Tyr Ile Ala Asp Pro Val Asn Val Glu
```

His Val Leu Lys Thr Asn Phe Thr Asn Tyr Pro Lys Gly Asp Val Tyr
20 25 30

```
Arg Ser Tyr Met Asp V: Leu Leu Gly Asp Gly Ile Phe Asn Ala Asp
         35
Gly Glu Leu Trp Arg Lys Gln Arg Lys Thr Ala Ser Phe Glu Phe Ala
Ser Lys Asn Leu Arg Asp Phe Ser Ala Asn Val Phe Arg Glu Tyr Ser
                     70
                                         75
Leu Lys Leu Ser Gly Ile Leu Ser Gln Ala Ser Lys Ala Gly Lys Val
Val Asp Met Gln Glu Leu Tyr Met Arg Met Thr Leu Asp Ser Ile Cys
                                105
Xaa Val Gly Phe Gly Val Xaa Ile Gly Thr Leu Ser Pro Asp Leu Pro
        115
                            120
Glu Asn Ser Phe Xaa Gln Ala Phe Asp Ala Ala Asn Ile Ile Val Thr
                        135
Leu Arg Phe Ile His Pro Leu Trp Arg Ile Gln Lys Phe Phe
145
                    150
<210> 5
<211> 1092
<212> DNA
<213> Zea mays
<400> 5
gaatteeaag egaggeeett gtageagaga gtgttgetga tgeagtegge ggaaatgagt 60
gegtgetgag ageaacgetg aggggtteea gggatggeaa tggetatgge aateggetag 120
aggtggagga caaggtggtg aggattggga gggcaaccta tggcaagttg gtgaagaggc 180
acgcaatgag agatctattc agacttacac tggatgccgc caacaaattc aacctttaga 240
ttttgatact gtcactccta ctttattcct tggttgggca acttccaata ggctcatgtt 300
aatcaatgat tagtgattat tcagcaaata ttcttgtttg tttgacattt ataatatgtg 360
gggtgagacg gattaaatat catccatgag agctttatct tcatgctctc ttgatttttgg 420
tttcagatca ttctttcagt gttcacaaga attttctcag tttggtccat gtaatttttg 480
aagtgaggtt cettaaattt cattatgett eettetttt etagactage aactgeatga 540
cttttcactt tgqqttcaca aattqactca caaqaaaaca aattcacttt tgqqttcaca 600
aatteetett eaggatgtae titteacitg aactgteatg tataggaaca aggaatgget 660
cagtttttaa ggaacaatgt acagatttca tttcagaact ctttctggtt ggttgagttt 720
cagacttttt gtaccaaget gatggateac aatacttgtt tecaaagtet gataacagaa 780
actggcaact cctaattgat aataaaaaga ataaaataca gtatcagata tctcattttc 840
ttggttggca gatcacaaaa aggaacacaa aggctaagcc tcctacttgt tcgggagtta 900
ggtcagggac accatatgaa tqaaaqaaat cttaatttgg qqtcacacca aqattqtctc 960
tctcgaggtt ggggggtccc taaggttggt agtagcaata cccaatatat cacctaacaa 1020
acccaatcca tgctacatac atacatagca tccatcactt gtagactgga cccttcatca 1080
agagcaccat gg
                                                                   1092
```

```
<210> 6
```

<sup>&</sup>lt;211> 267

<sup>&</sup>lt;212> DNA

<sup>&</sup>lt;213> Zea mays

```
<400> 6
ccccatctca ttttcttggt tggcagatca caaaaaggaa cacaaagget aagectecta 60
cttgttcggg agttaggtca gggacaccat atgaatgaaa gaaatcttaa tttqqqqtca 120
caccaagatt gtctctctcg aggttggggg gtccctaagg ttggtagtag caatacccaa 180
tatatcacct aacaaaccca atccatgcta catacataca tagcatccat cacttgtaga 240
ctggaccctt catcaagagc accatgg
<210> 7
<211> 3897
<212> DNA
<213> Zea mays
<400> 7
gaattecaag cgaggeeett gtagcagaga gtgttgetga tgcagtegge ggaaatgagt 60
gegtgetgag ageaacgetg aggggtteca gqqatqqcaa tgqctatqqc aategqctaq 120
aggtggagga caaggtggtg aggattggga gggcaaccta tggcaagttg gtgaagaggc 180
acgcaatgag agatetatte agacttacae tggatgeege caacaaatte aacetttaga 240
ttttgatact gtcactccta ctttattcct tggttgggca acttccaata ggctcatgtt 300
aatcaatgat tagtgattat tcagcaaata ttcttgtttg tttgacattt ataatatgtg 360
gggtgagacg gattaaatat catccatgag agctttatct tcatqctctc ttqattttqg 420
tttcagatca ttctttcagt gttcacaaga attttctcag tttggtccat gtaatttttg 480
aagtgaggtt cettaaattt cattatgett cetttetttt etagaetage aactgeatga 540
cttttcactt tgggttcaca aattgactca caagaaaaca aattcacttt tgggttcaca 600
aatteetett caggatgtae tttteacttg aactgteatg tataggaaca aggaatgget 660
cagtttttaa ggaacaatgt acagatttca tttcagaact ctttctggtt ggttgagttt 720
cagacttttt gtaccaaget gatggateac aatacttgtt tecaaagtet gataacagaa 780
actggcaact cctaattgat aataaaaaga ataaaataca gtatcagata tctcattttc 840
ttggttggca gatcacaaaa aggaacacaa aggctaagcc tcctacttgt tcgggagtta 900
ggtcagggac accatatgaa tgaaagaaat ettaatttgg ggtcacacca agattgtctc 960
tctcgaggtt ggggggtccc taaggttggt agtagcaata cccaatatat cacctaacaa 1020
acceaateca tgetacatac atacatagea tecateaett gtagactgga ceetteatea 1080
agageaceat ggaggaaget cacateaege eggegaegee ategeeatte tteecaetag 1140
cagggeetea caagtacate gegeteetee tggttgteet etcatggate etggtecaga 1200
ggtggagcct gaggaagcag aaaggcccga gatcatggcc agtcatcggt gcaacggtgg 1260
agcagetgag gaactaccae eggatgeaeg aetggettgt egggtacetg teaeggeaea 1320
ggacagtgac cgtcgacatg ccgttcactt cctacaccta catcgctgac ccggtgaatq 1380
tegageatgt ceteaagaet aactteaeea attaceeeaa ggtaaatgae etgaaeteae 1440
tgatgttcag tcttcggaaa tcagagctga aagctgaatc gaatgtgcct gaacaccqtg 1500
tagggaateg tgtacagate ctacatggac gtgetecteg gtgacggcat cttcaacgcc 1560
gacggcgagc tgtggaggaa gcagaggaaq acggcgaqtt tcqaqttcqc ctccaaqaac 1620
ctgagggatt tcagcgccat tgtgttcaga gagtactccc tgaagctgtc gggtatactg 1680
agccaggcat ccaaggcagg caaagttgtg gacatgcagg tgagatcact gctcccttgc 1740
cattgccaac atgagcattt caacctgaga cacqaqaqct accttqccqa ttcaqqaact 1800
ttacatgagg atgacgctgg actocatetg caaggttggg tteggggtcg agateggcae 1860
getgtegeeg gateteeceg agaacagett egegeaggeg ttegatgeeg ecaacateat 1920
egteacgetg eggtteateg accegetgtg gegeateaag aggttettee aegtegggte 1980
agaggecete etagegeaga geateaaget egtggaegag tteacetaca gegtgateeg 2040
ccggaggaag gccgagatcg tcgaggcccg ggccagcggc aaacaggaga aggtacgtgc 2100
acatgactgt ttcgattctt cagttcatcg tcttggccgg gatggacctg atcctgattg 2160
attatatatc cgtgtgactt gtgaggacaa attaaaatgg gcagatgaag cacgacatcc 2220
tgtcacggtt catcgagcta ggcgaggccg gcgacgacgg cggcggcttc ggggacgaca 2280
agageeteeg ggaegtggtg eteaaetteg tgategeegg gegggaeaeg aeggegaega 2340
egetgtegtg gtteaegeae atggeeatgt cecaecegga egtggeegag aagetgegee 2400
gegagetgtg egegttegag geggagegeg egegegagga gggegtegeg etegtgeeet 2460
geggeggege tgaegeegae gaeaaggegt tegeegeeeg egtggegeag ttegegggee 2520
```

tecteaceta egacageete ggeaagetgg tetaceteea egeetgegte acegagaege 2580 teegeetgta eeeegeegte eeteaggtga gegegeeega eaegegaeet eeggteeaga 2640

gcacagcatg	cagtgagtgg	ctgaatgc	aatgcacatg	cacttgcgcg	cgcgcaggac	2700
cccaagggga	tcctggagga	cgacgtgctg	ccggacggga	cgaaggtgag	ggccggcggg	2760
atggtgacgt	acgtgcccta	ctcgatgggg	cggatggagt	acaactgggg	ccccgacgcg	2820
gcgagettcc	ggccggagcg	gtggatcaac	gaggatggcg	cgttccgcaa	cgcgtcgccg	2880
ttcaagttca	cggcgttcca	ggcggggccg	aggatctgcc	tgggcaagga	ctcggcgtac	2940
ctgcagatga	agatggcgct	ggccatcctc	ttgcgcttct	acagetteeg	gctgctggag	3000
gggcacccgg	tgcagtaccg	catgatgacc	atcctctcca	tggcgcacgg	cctcaaggtc	3060
cgcgtctcta	gggccgtctg	atgtcatggc	gatttgggat	atcatcccgc	ttaatcctta	3120
aaaatttgca	tgcatgcatg	taagggaaag	cgatgggttt	cattggtggc	ttggcttaag	3180
ccttaaaaac	tccgtcgggt	cttgcgaacc	accacatcac	tagtgttttg	tactctactc	3240
ctcagtggaa	gtgtagtgac	agcatacaag	ttcatcatat	atattatcct	ctttcttcgc	3300
cggatgcttc	ccgggacctt	ttggagacca	ttactgacag	gcgtgtgaaa	aaaaggcttc	3360
ttctgcggcg	aagttttggg	ttcagagtct	tggcgtcttt	gcagcagaaa	aaaggtttgg	3420
aaggatctga	accctgaacc	gaaaatggct	tcggaaatat	gctcgcatcg	gggcggggcc	3480
gtcactcggg	atgacgacaa	gcccacaagc	agtgagagcg	aagcgatctt	tggagtttgg	3540
agacactctc	ggacccctcg	gcgctccgcg	agctcatctt	cgcctcctct	gtcgtgtccg	3600
	gegeeegeee		_			3660
	ctcatccgcg					3720
	tggtattgta				-	3780
	tcaaaattga					3840
agaatgagag	acaacccaaa	ggttagagat	gaaataagct	gagtaaacga	cgaattc	3897